

PATENT  
930008-2003AMENDMENT

Kindly amend the application as follows:

IN THE CLAIMS:

Kindly cancel claims 1, 2, and 15-23 and re-write claims 10-14, 22-27 and 30-33 as follows:

10. (Once Amended) Kit according to claim 9, wherein the nucleic acid molecule is from 10 to 250, preferably from 15 to 30, nucleotides long, especially characterized in that it is the nucleic acid molecule having the sequence SEQ ID NO 5.

11. (Twice Amended) Kit according to claim 1, wherein the nucleic acid molecule is single-stranded or double-stranded.

12. (Twice Amended) Kit according to claim 1, wherein the nucleic acid molecule is present

- (i) as DNA, or
- (ii) as RNA corresponding to (i), or
- (iii) as PNA,

the nucleic acid molecule, where appropriate, being modified in a manner known *per se* for analytical detection methods, especially methods based on hybridisation and/or amplification.

13. (Once Amended) Kit according to claim 12, wherein the nucleic acid molecule is modified by the replacement of up to 10% of the nucleotides, especially 1 or 2 nucleotides, by analogous components known *per se* for probes and/or primers, especially by nucleotides that do not occur naturally in bacteria.

14. (Twice Amended) Kit according to claim 12, wherein the nucleic acid molecule is modified or labelled or is additionally modified or labelled in that it comprises, in a manner known *per se* for analytical detection methods, one or more radioactive groups, coloured groups, fluorescent groups, groups for immobilisation on a solid phase and/or groups for an indirect or direct reaction, especially an enzymatic reaction, especially using antibodies, antigens, enzymes and/or substances having an affinity for enzymes or enzyme complexes, or it comprises, in a manner

PATENT  
930008-2003

ε<sup>1</sup>  
Cord. known *per se* for analytical detection methods, groups that have been modified or that modify in some other manner.

24. (Once Amended) Nucleic acid molecule that hybridises selectively to RNA or DNA of a group of bacteria of the genus *Staphylococcus*, wherein it contains at least 10 successive nucleotides of the region from

- (i) nucleotide position 54 to 83 of SEQ ID NO 1, or
- (ii) nucleotide position 100 to 166 of SEQ ID NO 1, or
- (iii) the sequences complementary to (i) or (ii), excluding a nucleic acid molecule that has a sequence according to Figures 1 to 10.

ε<sup>2</sup>  
25. (Once Amended) Nucleic acid molecule for the detection of the presence or absence of bacteria belonging to a group of bacteria of the genus *Staphylococcus*, wherein it makes it possible by means of nucleic acid hybridisation and/or nucleic acid amplification methods under suitable reaction conditions to distinguish between bacteria to be detected and bacteria that are not to be detected and that the distinction is possible by virtue of a differing nucleic acid sequence at at least one base position in the region of SEQ ID NO: 1; or of its complementary sequence, in the genomic DNA and/or RNA of bacteria to be detected and bacteria that are not to be detected, excluding a nucleic acid molecule that has a sequence according to Figures 1 to 10.

26. (Once Amended) Nucleic acid molecule for the detection of the presence or absence of bacteria belonging to a group of bacteria of the genus *Staphylococcus*, wherein it makes it possible by means of nucleic acid hybridisation and/or nucleic acid amplification methods under reaction conditions known *per se* to distinguish between bacteria to be detected and bacteria that are not to be detected and that the distinction is possible by virtue of a differing nucleic acid sequence at at least one base position in

- (i) the region 54 to 83 of SEQ ID NO 1, or
- (ii) the region 100 to 166 of SEQ ID NO 1, or
- (iii) the sequence that is complementary to (i) or (ii), in the genomic DNA and/or RNA of bacteria to be detected and bacteria that are not to be detected, excluding a nucleic acid molecule that has a sequence according to Figures 1 to 10.

PATENT  
930008-2003

ε<sup>2</sup>  
corel. 27. (Once Amended) Nucleic acid molecule, wherein it has the SEQ ID NO 1 or its complementary sequence.

---

30. (Twice Amended) Nucleic acid molecule, wherein its sequence in at least 10 successive nucleotides of its nucleotide chain

- ε<sup>3</sup>
- (i) is identical to a nucleic acid molecule according to claim 22, or
  - (ii) corresponds in 9 out of 10 successive nucleotides to a nucleic acid molecule according to claim 22, or
  - (iii) corresponds in 8 out of 10 successive nucleotides to a nucleic acid molecule according to claim 22, or
  - (iv) is at least 90% homologous to a nucleic acid molecule according to claim 22.

31. (Once Amended) Nucleic acid molecule, wherein it has the SEQ ID NO 5 or its complementary sequence.

32. (Twice Amended) Nucleic acid molecule according to claim 22, wherein it is from 10 to 250, preferably from 15 to 30, nucleotides long.

33. (Twice Amended) Nucleic acid molecule according to claim 22, wherein the nucleic acid molecule is single-stranded or double-stranded.

---

Kindly add new claims 34-51 as follows:

---

ε<sup>4</sup> 34. (New) A method for the detection of the presence or absence of bacteria of the genus *Staphylococcus*, which method comprises amplifying RNA or DNA in a polymerase chain reaction (PCR), with a primer or probe which hybridizes selectively to at least 10 successive nucleotides of the region from

- (i) nucleotide position 54 to 83 of SEQ ID NO 1, or
- (ii) nucleotide position 100 to 166 of SEQ ID NO 1, or
- (iii) the sequences complementary to (i) or (ii).

35. (New) The method according to claim 34, wherein the bacteria of the genus *Staphylococcus* comprises various strains of *Staphylococcus aureus*.

PATENT  
930008-2003

36. (New) The method according to claim 34, wherein the bacteria of the genus *Staphylococcus* comprises exclusively *Staphylococcus aureus* strains.

37. (New) A method for the detection of the presence or absence of bacteria of the genus *Staphylococcus*, which method comprises amplifying RNA or DNA in polymerase chain reaction (PCR), wherein at least one nucleic acid molecule as a primer and/or probe under suitable reaction conditions distinguishes between bacteria to be detected and bacteria that are not to be detected, and wherein the distinction is possible by virtue of a differing nucleic acid sequence at least one base position in the region of SEQ ID NO: 1, or of its complementary sequence, in the genomic DNA and/or RNA of bacteria to be detected and bacteria that are not to be detected.

38. (New) The method according to claim 37, wherein the bacteria of the genus *Staphylococcus* comprises various strains of *Staphylococcus aureus*.

39. (New) The method according to claim 37, wherein the bacteria of the genus *Staphylococcus* comprises exclusively *Staphylococcus aureus* strains.

40. (New) A method for the detection of the presence or absence of bacteria of the genus *Staphylococcus*, which method comprises amplifying RNA or DNA in polymerase chain reaction (PCR), wherein at least one nucleic acid molecule as a primer and/or probe under reaction conditions known *per se* distinguishes between bacteria to be detected and bacteria that are not to be detected, distinction is possible by virtue of a differing nucleic acid sequence at least one base position in

(i) the region 54 to 83 of SEQ ID NO 1, or

(ii) the region 100 to 166 of SEQ ID NO 1, or

(iii) the sequence that is complementary to the region according to (i) or (ii) in the genomic DNA and/or RNA of bacteria to be detected and bacteria that are not to be detected.

41. (New) The method according to claim 40, wherein the bacteria of the genus *Staphylococcus* comprises various strains of *Staphylococcus aureus*.

PATENT  
930008-2003

42. (New) The method according to claim 40, wherein the bacteria of the genus *Staphylococcus* comprises exclusively *Staphylococcus aureus* strains.

43. (New) A method for the detection of the presence or absence of bacteria of the genus *Staphylococcus*, which method comprises hybridizing RNA or DNA by means of nucleic acid hybridization, with a primer or probe which hybridizes selectively to at least 10 successive nucleotides of the region from

- (i) nucleotide position 54 to 83 of SEQ ID NO 1, or
- (ii) nucleotide position 100 to 166 of SEQ ID NO 1, or
- (iii) the sequences complementary to (i) or (ii).

44. (New) The method according to claim 43, wherein the bacteria of the genus *Staphylococcus* comprises various strains of *Staphylococcus aureus*.

ε4  
cont. 45. (New) The method according to claim 43, wherein the bacteria of the genus *Staphylococcus* comprises exclusively *Staphylococcus aureus* strains.

46. (New) A method for the detection of the presence or absence of bacteria of the genus *Staphylococcus* by means of nucleic acid hybridization, wherein at least one nucleic acid molecule as primer and/or probe under suitable reaction conditions distinguishes between bacteria to be detected and bacteria that are not to be detected, and wherein the distinction is possible by virtue of a differing nucleic acid sequence at least one base position in the region of SEQ ID NO: 1, or of its complementary sequence, in the genomic DNA and/or RNA of bacteria to be detected and bacteria that are not to be detected.

47. (New) The method according to claim 46, wherein the bacteria of the genus *Staphylococcus* comprises various strains of *Staphylococcus aureus*.

48. (New) The method according to claim 46, wherein the bacteria of the genus *Staphylococcus* comprises exclusively *Staphylococcus aureus* strains.

PATENT  
930008-2003

49. (New) A method for the detection of the presence or absence of bacteria of the genus *Staphylococcus* by means of nucleic acid hybridization wherein at least one nucleic acid molecule as primer and/or probe under reaction conditions known *per se* distinguishes between bacteria to be detected and bacteria that are not to be detected, distinction is possible by virtue of a differing nucleic acid sequence at least one base position in

(i) the region 54 to 83 of SEQ ID NO 1, or

(ii) the region 100 to 166 of SEQ ID NO 1, or

(iii) the sequence that is complementary to the region according to (i) or (ii)

in the genomic DNA and/or RNA of bacteria to be detected and bacteria that are not to be detected.

50. (New) The method according to claim 49, wherein the bacteria of the genus *Staphylococcus* comprises various strains of *Staphylococcus aureus*.

51. (New) The method according to claim 49, wherein the bacteria of the genus *Staphylococcus* comprises exclusively *Staphylococcus aureus* strains.